09/989994
File 5:Biosis Previews(R) 1969-2004/Mar W1
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Set Items Description
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Set	Items	Description
S1	154	AU='LIU QIANG'
S2	7054	ZINC()FINGER
S3	7	S1 AND S2
S4	0	DRSNLTR AND TSGHLSR AND RSDHLSR
S5	0	DSNLTR

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3/7/1
DIALOG(R)File 5:Biosis Previews(R)

0014165006 BIOSIS NO.: 200300122116
Methods of using randomized libraries of %%%zinc%%% %%%finger%%% proteins for the identification of gene function
AUTHOR: Case Casey C (Reprint); %%%Liu Qiang%%%; Rebar Edward J; Wolffe Alan P
AUTHOR ADDRESS: San Mateo, CA, USA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office Patents 1266 (1): Jan. 7, 2003 2003
MEDIUM: e-file
ISSN: 0098-1133 _(ISSN print)
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The present invention relates to methods of using libraries of randomized %%%zinc%%% %%%finger%%% proteins to identify genes associated with selected phenotypes.

3/7/2
DIALOG(R)File 5:Biosis Previews(R)

0013591660 BIOSIS NO.: 200200185171
Validated %%%zinc%%% %%%finger%%% protein designs for all 16 GNN DNA triplet targets
AUTHOR: %%%Liu Qiang%%%; Xia ZhenQin; Case Casey C (Reprint
AUTHOR ADDRESS: Point Richmond Technical Center, Sangamo BioSciences Inc., Richmond, CA, 94804, USA**USA
JOURNAL: Journal of Biological Chemistry 277 (6): p3850-3856 February 8, 2002 2002
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Cys2-His2-type %%%zinc%%% %%%finger%%% DNA-binding proteins

can be engineered to bind specifically to many different DNA sequences. A single %%%zinc%%% %%%finger%%% typically binds to a 3-4-base pair DNA subsite. One strategy for design is to identify highly specific fingers that recognize each of the 64 possible DNA triplets. We started with a subgroup of the 64 triplets, the GNN-binding fingers. The GNN-binding fingers have been examined in several studies, but previous studies did not produce specific fingers for all of the 16 GNN triplets. These previous studies did not provide any information on the possible positional or context effects on the performance of these fingers. To identify the most specific design and take the possible positional effects into consideration, we did a large-scale site selection experiment on our GNN designs. From this study, we identified very specific fingers for 14 of the 16 GNN triplets, demonstrating for the first time a clear positional dependence for many of the designs. Further systematic specificity study reveals that the in vivo functionality of these %%%zinc%%% %%%finger%%% proteins in a reporter assay depends on their binding affinities to their target sequences, thus giving a better understanding of how these %%%zinc%%% %%%finger%%% proteins might function inside cells.

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DIALOG(R)File 5:Biosis Previews(R)

0013256071 BIOSIS NO.: 200100427910
Regulation of the endogenous VEGF-A chromosomal locus using designed %%%zinc%%% %%%finger%%% proteins
AUTHOR: Liu Pei-Qi (Reprint); Rebar Edward J (Reprint); Zhang Lei (Reprint); %%%Liu Qiang%%% (Reprint); Jamieson Andrew C (Reprint); Liang Yuxin (Reprint); Qi Hong (Reprint); Li Pei-Xiang (Reprint); Chen Bingliang (Reprint); Mendel Matthew C (Reprint); Zhong Xiaohong (Reprint); Lee Ya-Li (Reprint); Eisenberg Steve (Reprint); Spratt S Kaye (Reprint); Case Casey C (Reprint); Wolffe Alan P (Reprint
AUTHOR ADDRESS: Sangamo BioSciences, 501 Canal Blvd., Suite A100, Richmond, CA, 94804, USA**USA
JOURNAL: Biochemistry and Cell Biology 79 (3): p377 2001 2001
MEDIUM: print
CONFERENCE/MEETING: 22nd Annual West Coast Chromatin and Chromosomes Conference Pacific Grove, California, USA December 07-10, 2000; 20001207
ISSN: 0829-8211
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

3/7/4
DIALOG(R)File 5:Biosis Previews(R)

0013256047 BIOSIS NO.: 200100427886
Synthetic %%%zinc%%% %%%finger%%% transcription factor action at an endogenous chromosomal site: Activation of the human erythropoietin gene
AUTHOR: Zhang Lei (Reprint); Spratt S Kaye (Reprint); %%%Liu Qiang%%% (Reprint); Johnstone Brian (Reprint); Qi Hong (Reprint); Raschke Eva E (Reprint); Jamieson Andrew C (Reprint); Rebar Edward J (Reprint); Wolffe Alan P (Reprint); Case Casey C (Reprint

AUTHOR ADDRESS: Sangamo BioSciences, Point Richmond Tech Center, 501 Canal Boulevard, Suite A100, Richmond, CA, 94804, USA**USA
JOURNAL: Biochemistry and Cell Biology 79 (3): p365 2001 2001
MEDIUM: print
CONFERENCE/MEETING: 22nd Annual West Coast Chromatin and Chromosomes Conference Pacific Grove, California, USA December 07-10, 2000; 20001207
ISSN: 0829-8211
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

3/7/5
DIALOG(R)File 5:Biosis Previews(R)

0013072090 BIOSIS NO.: 200100243929
Regulation of an endogenous locus using a panel of designed %%%zinc%%% %%%finger%%% proteins targeted to accessible chromatin regions: Activation of vascular endothelial growth factor A
AUTHOR: Liu Pei-Qi; Rebar Edward J; Zhang Lei; %%%Liu Qiang%%%; Jamieson Andrew C; Liang Yuxin; Qi Hong; Li Pei-Xiang; Chen Bingliang; Mendel Matthew C; Zhong Xiaohong; Lee Ya-Li; Eisenberg Stephen P; Spratt S Kaye; Case Casey C; Wolffe Alan P (Reprint
AUTHOR ADDRESS: Point Richmond Tech Center, Sangamo Bio-Sciences Inc., 501 Canal Blvd., Suite A100, Richmond, CA, 94804, USA**USA
JOURNAL: Journal of Biological Chemistry 276 (14): p11323-11334 April 6, 2001 2001
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have mapped conserved regions of enhanced DNase I accessibility within the endogenous chromosomal locus of vascular endothelial growth factor A (VEGF-A). Synthetic %%%zinc%%% %%%finger%%% protein (ZFP) transcription factors were designed to target DNA sequences contained within the DNase I-hypersensitive regions. These ZFPs, when fused to either VP16 or p65 transcriptional activation domains, were able to activate expression of the VEGF-A gene as assayed by mRNA accumulation and VEGF-A protein secretion through a range exceeding that induced by hypoxic stress. Importantly, multiple splice variants of VEGF-A mRNA with defined physiological functions were induced by a single engineered ZFP transcription factor. We present evidence for an enhanced activation of VEGF-A gene transcription by ZFP transcription factors fused to VP16 and p65 targeted to two distinct chromosomal sites >500 base pairs upstream or downstream of the transcription start site. Our strategy provides a novel approach for dissecting the requirements for gene regulation at a distance without altering the DNA sequence of the endogenous target locus.

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DIALOG(R)File 5:Biosis Previews(R)

0012855966 BIOSIS NO.: 200100027805
Synthetic %%%zinc%%% %%%finger%%% transcription factor action at an endogenous chromosomal site. Activation of the human erythropoietin gene
AUTHOR: Zhang Lei; Spratt S Kaye; %%%Liu Qiang%%%; Johnstone Brian; Qi Hong ; Raschke Eva E; Jamieson Andrew C; Rebar Edward J; Wolffe Alan P (Reprint); Case Casey C
AUTHOR ADDRESS: Point Richmond Tech Center, Sangamo BioSciences Inc., 501 Canal Blvd., Suite A100, Richmond, CA, 94804, USA**USA
JOURNAL: Journal of Biological Chemistry 275 (43): p33850-33860 October 27, 2000 2000
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have targeted the activation of an endogenous chromosomal locus including the human erythropoietin gene using synthetic transcription factors. These transcription factors are targeted to particular DNA sequences in the 5'-flanking region of the erythropoietin gene through engineering of a %%%zinc%%% %%%finger%%% DNA binding domain. The DNA binding domain is linked to a VP16 transcriptional activation domain. We find that these synthetic transcription factors invariably activate transiently transfected templates in which sequences within the 5' flank of the erythropoietin gene are fused to a luciferase reporter. The efficiency of activation under these circumstances at a defined site is dependent on DNA binding affinity. In contrast, only a subset of these same %%%zinc%%% %%%finger%%% proteins is able to activate the endogenous chromosomal locus. The activity of these proteins is influenced by their capacity to gain access to their recognition elements within the chromatin infrastructure. %%%Zinc%%% %%%finger%%% transcription factors will provide a powerful tool to probe the determinants of chromatin accessibility and remodeling within endogenous chromosomal loci.

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DIALOG(R)File 5:Biosis Previews(R)

0010960779 BIOSIS NO.: 199799594839
Design of polydactyl %%%zinc%%%-%%%finger%%% proteins for unique addressing within complex genomes
AUTHOR: %%%Liu Qiang%%%; Segal David J; Ghiara Jayant B; Barbas Carlos F III (Reprint
AUTHOR ADDRESS: Dep. Molecular Biol., BCC-515, Scripps Res. Inst., 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 94 (11): p5525-5530 1997 1997
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Zinc-ringer proteins of the Cys-2-His-2 type represent a class of malleable DNA-binding proteins that may be selected to bind diverse sequences. Typically, %%%zinc%%%-%%%finger%%% proteins containing three %%%zinc%%%-%%%finger%%% domains, like the murine transcription factor

Zif268 and the human transcription factor Sp1, bind nine contiguous base pairs. To create a class of proteins that would be generally applicable to target unique sites within complex genomes, we have utilized structure-based modeling to design a polypeptide linker that fuses two three-ringer proteins. Two six-ringered proteins were created and demonstrated to bind 18 contiguous bp of DNA in a sequence-specific fashion. Expression of these proteins as fusions to activation or repression domains allows transcription to be specifically up- or down-modulated within human cells. Polydactyl %%%zinc%%%-%%%finger%%% proteins should be broadly applicable as genome-specific transcriptional switches in gene therapy strategies and the development of novel transgenic plants and animals.

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